

Fig. 1A

APPROVED	O.G. FIG.	CLASS	SUBCLASS
BY DRAFTSMAN			

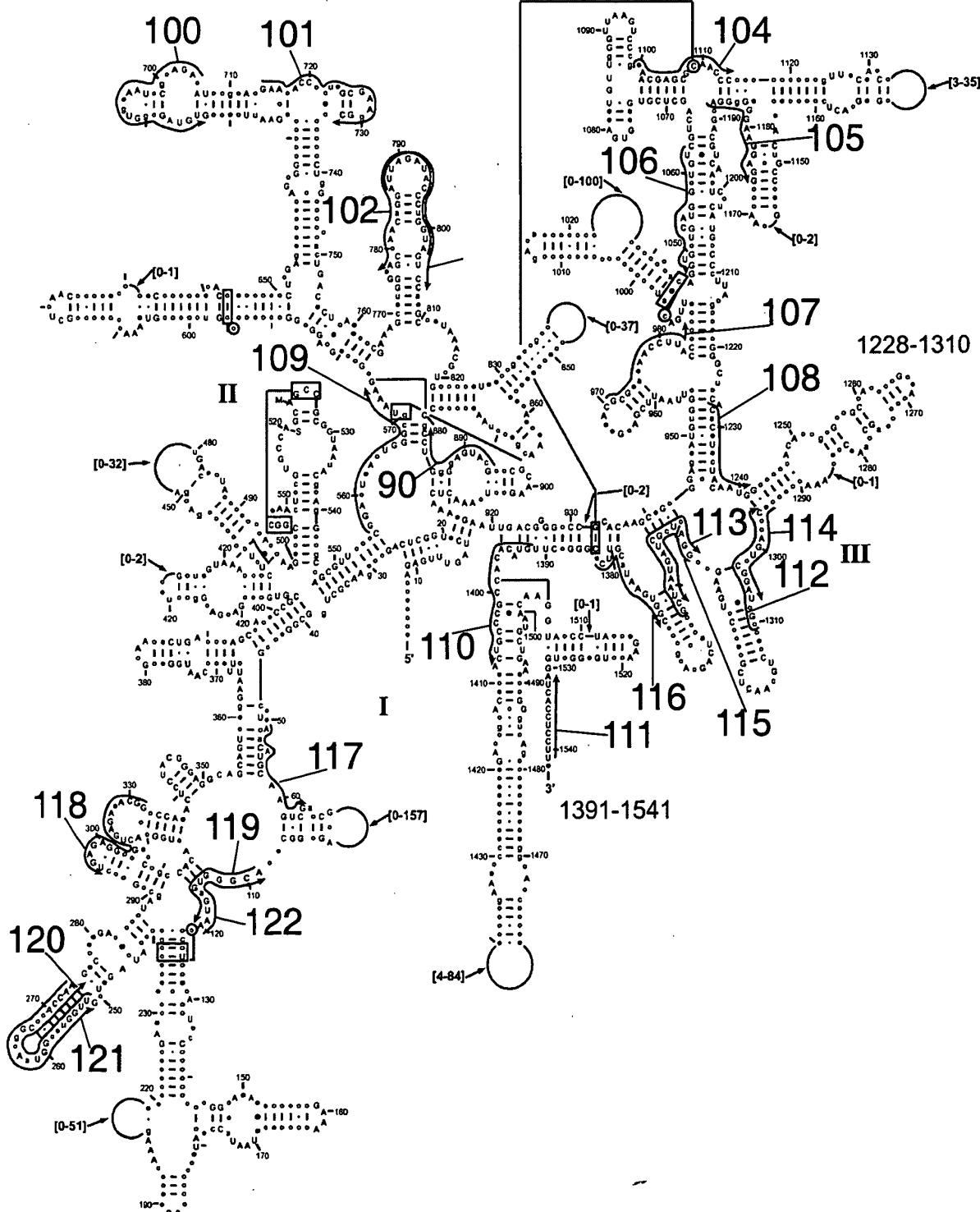


Fig. 1A-2

APPROVED	O.G. FIG.	CLASS	SUBCLASS
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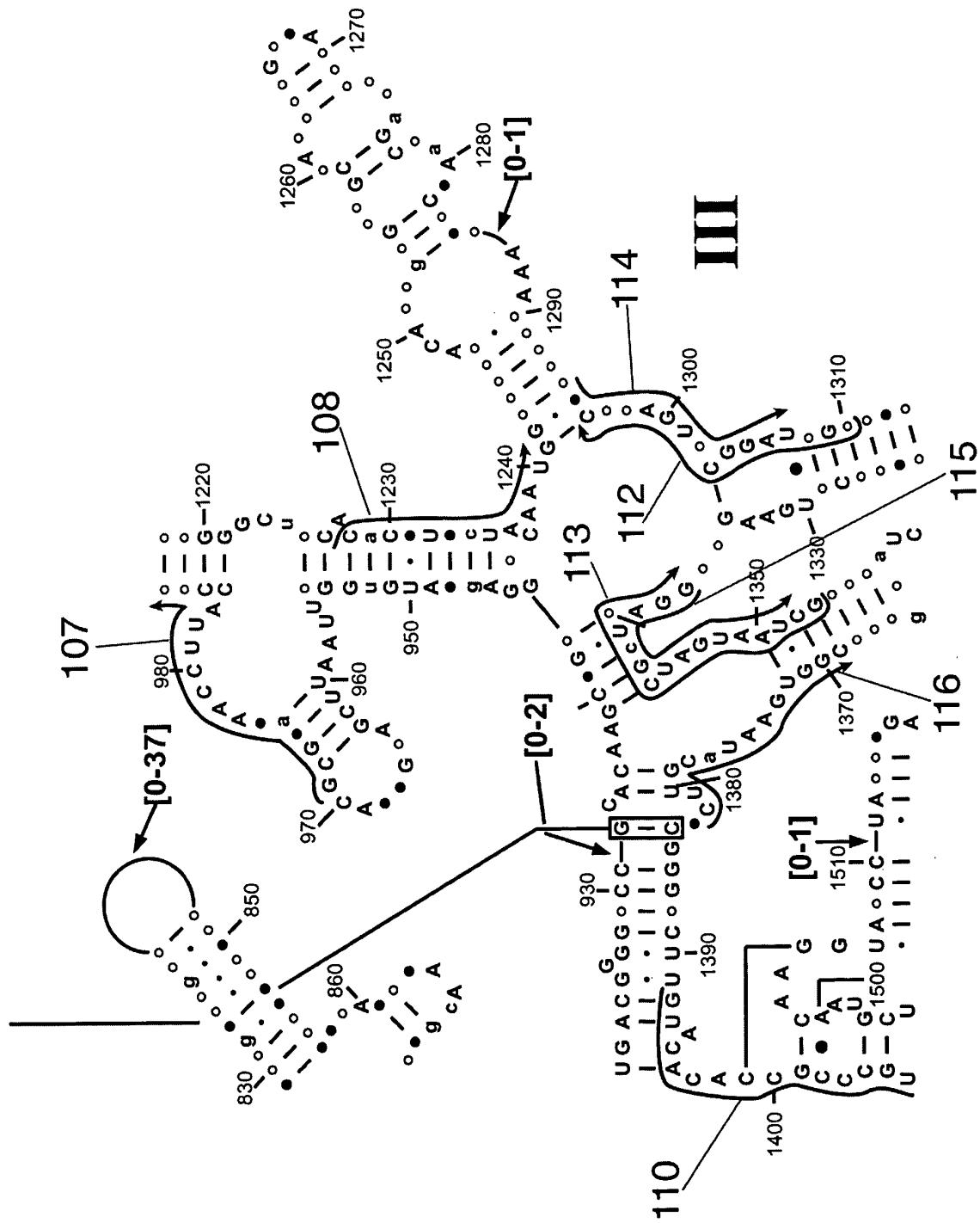


Fig. 1A-3

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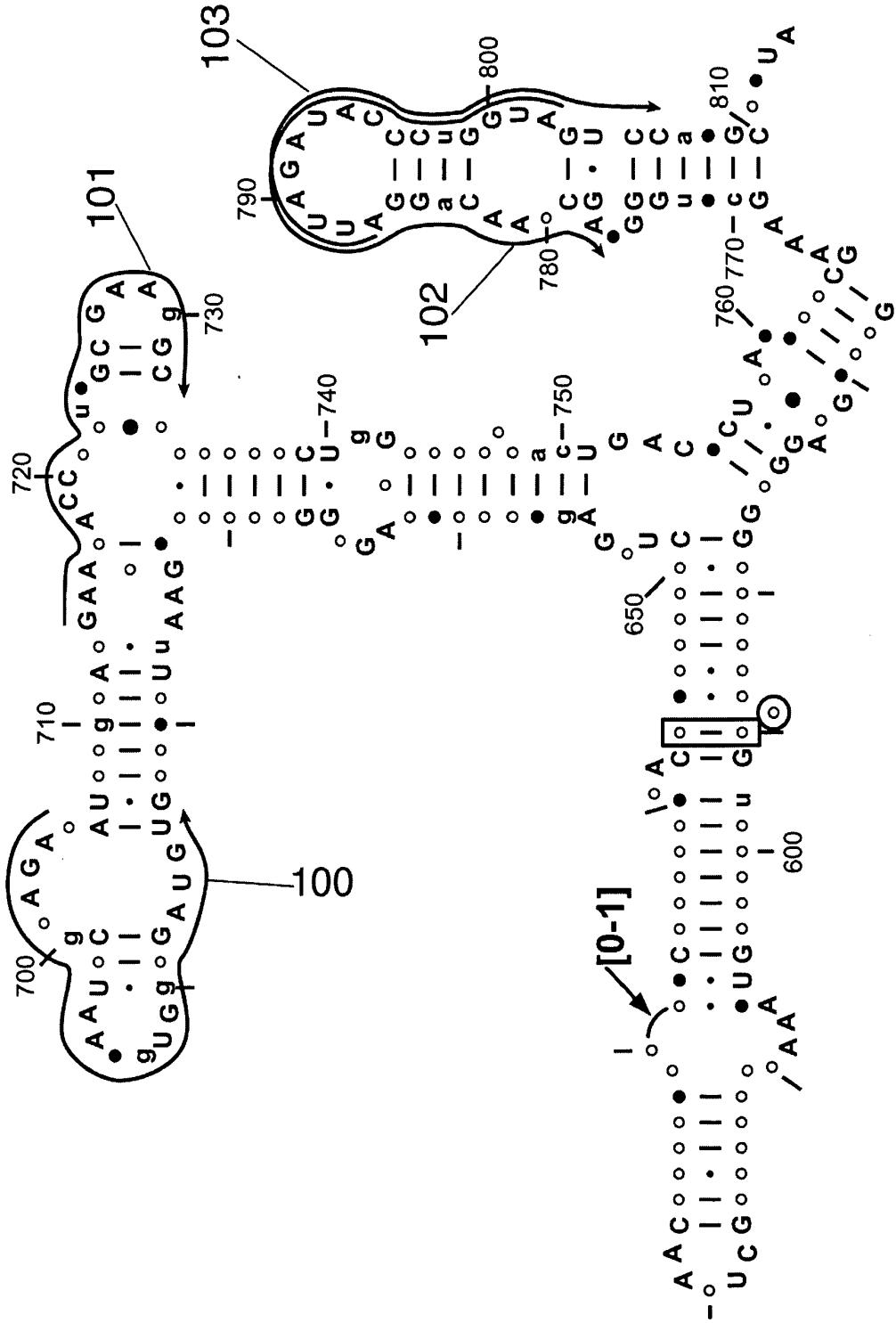


Fig. 1A-4

APPROVED	O.G. FIG.
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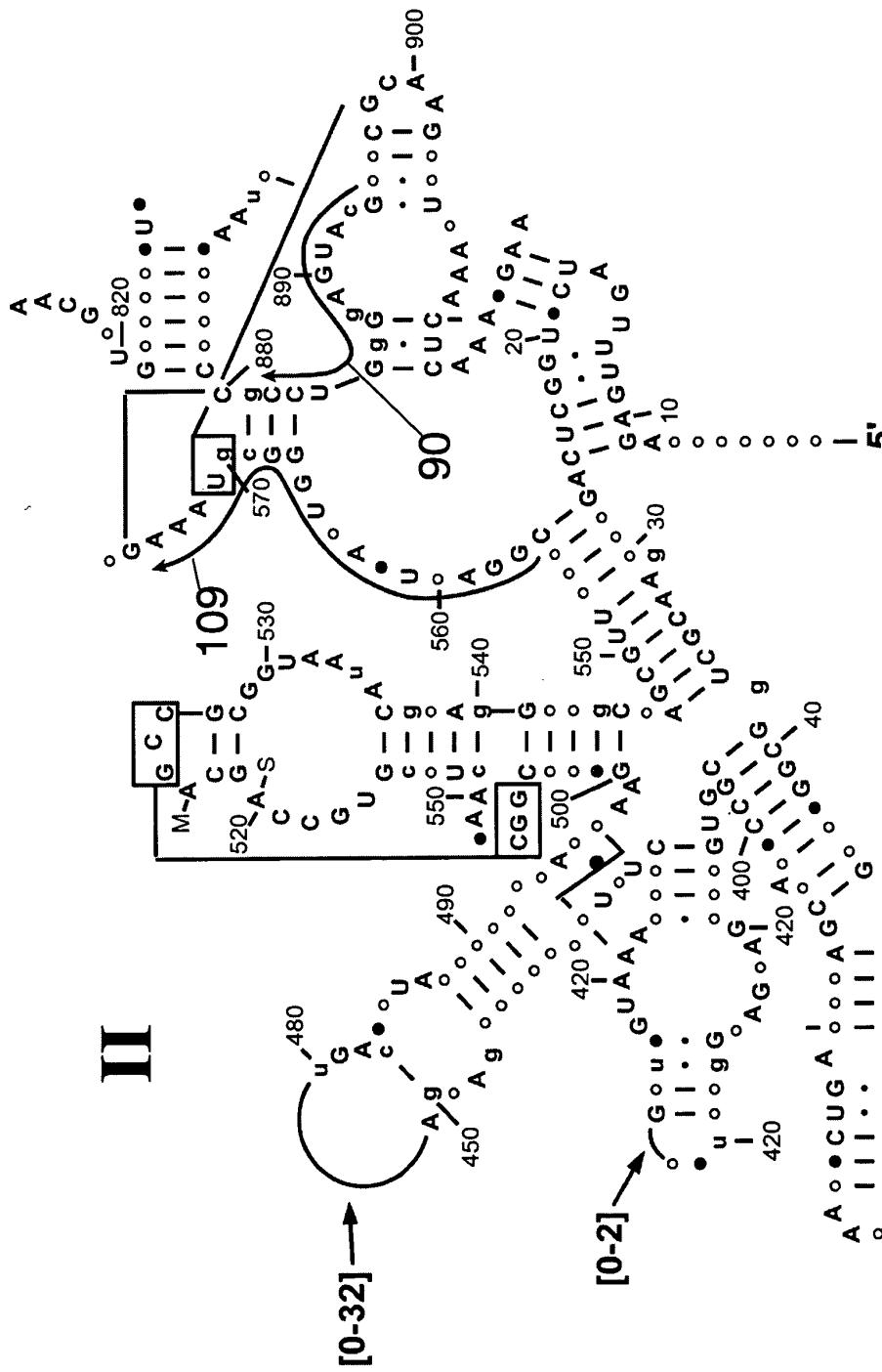


Fig. 1B-1

APPROVED	O. G. FIG.	
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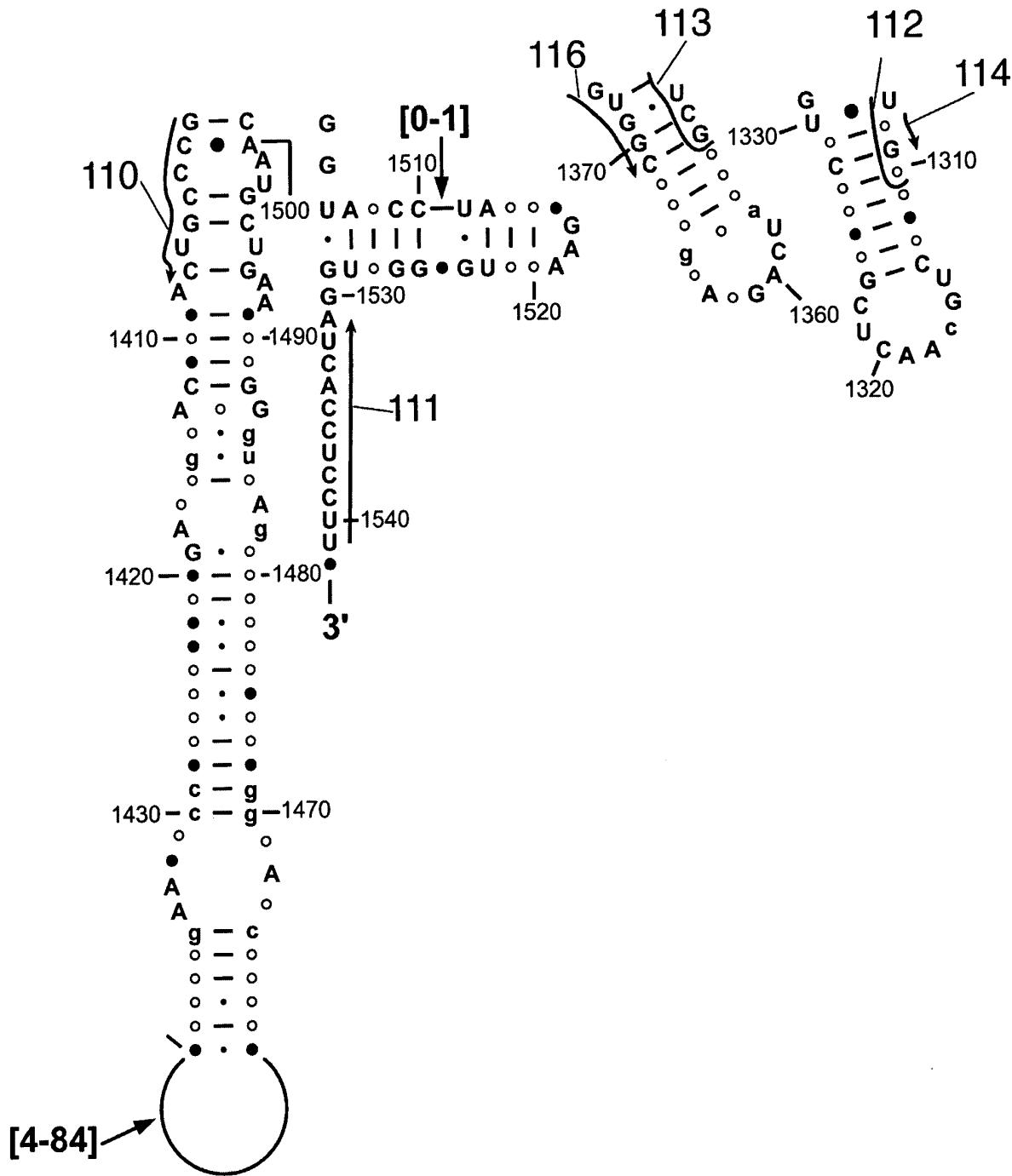


Fig. 1B-2

APPROVED	O. G. FIG.
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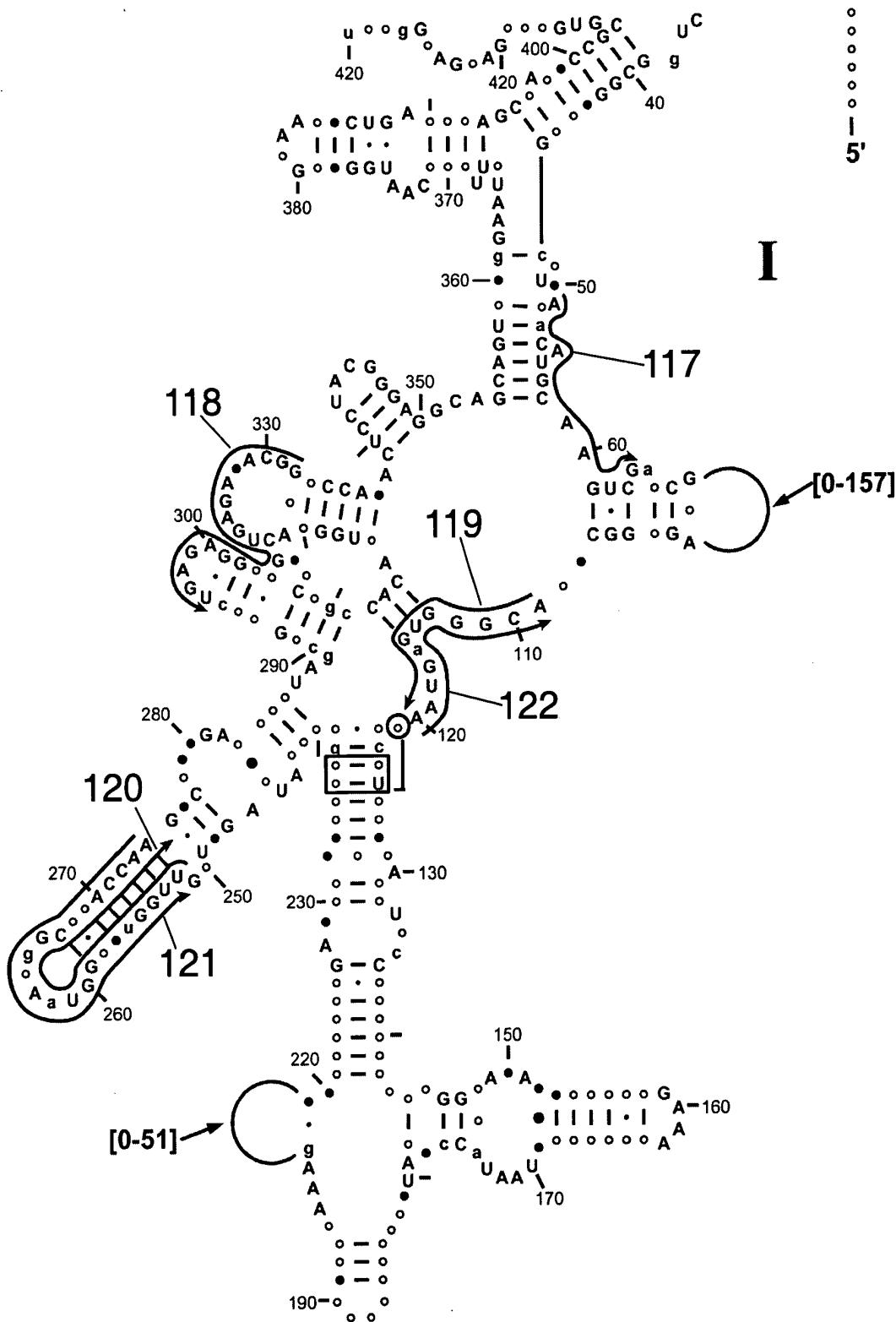


Fig. 1C-1

APPROVED	O.G. FIG.
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DRAFTSMAN	CLASS

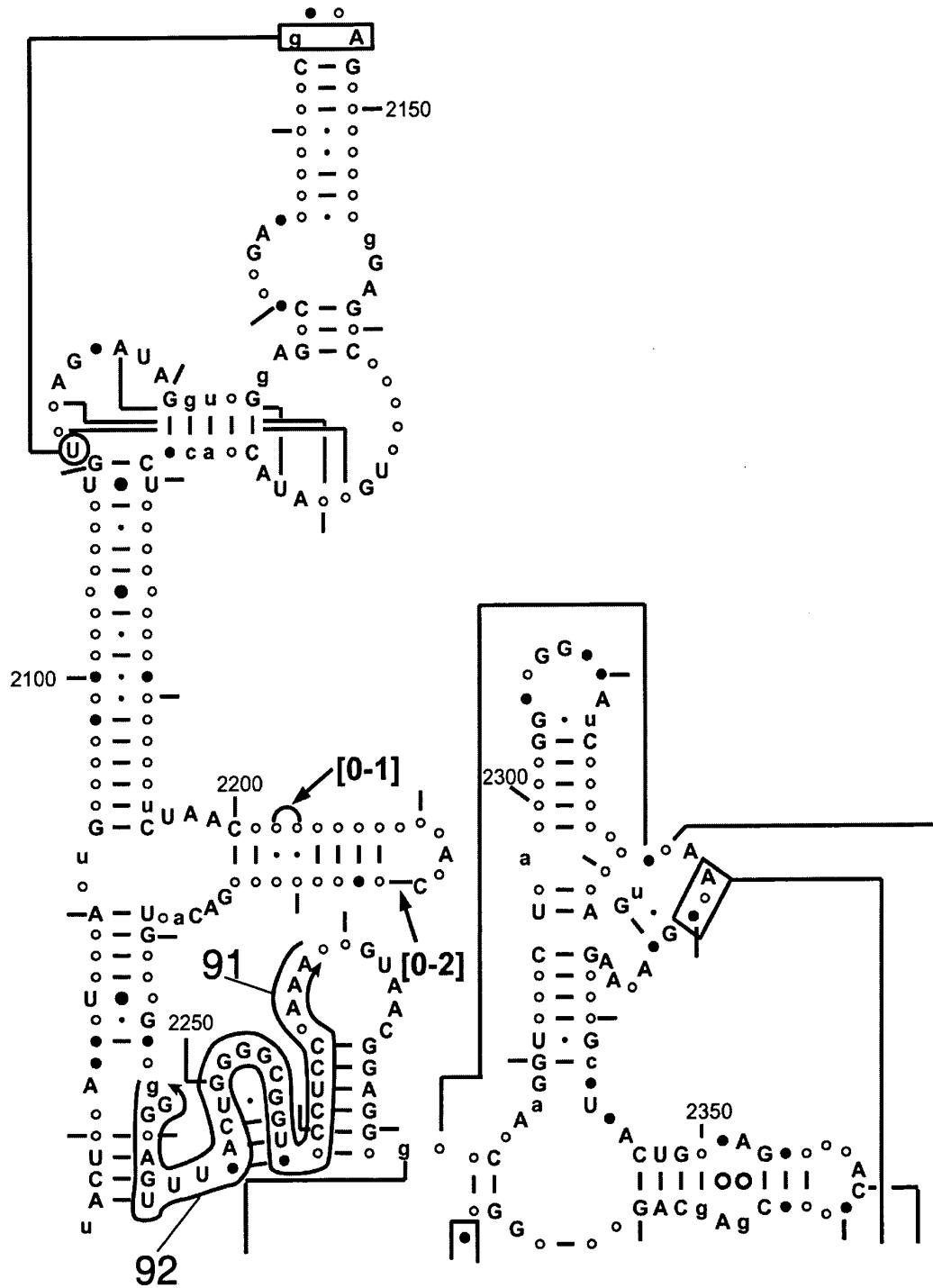


Fig. 1C-2

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Note: TA in *E. coli* replaced with CC so that the reverse complement becomes GG to match with predominant YY

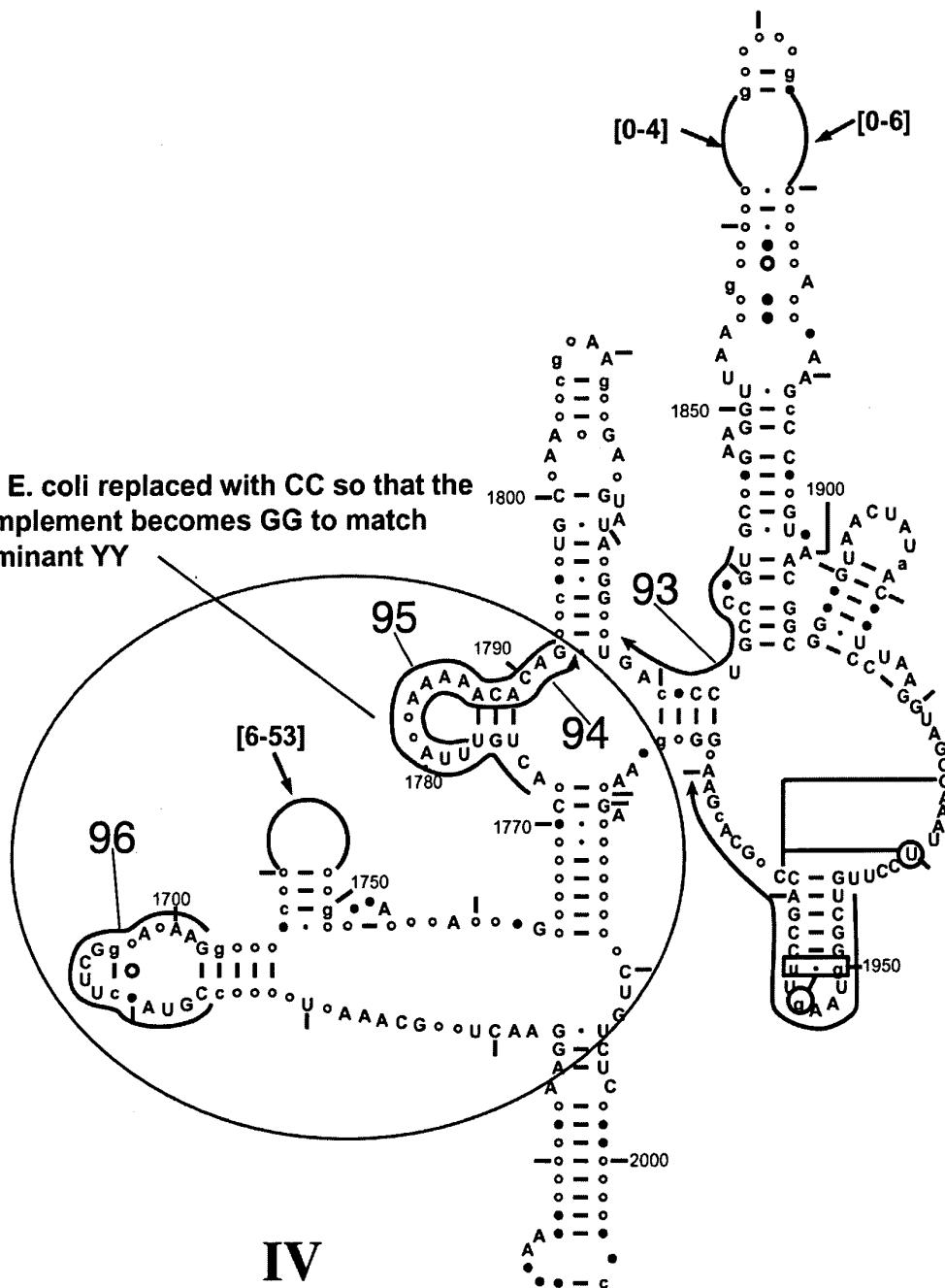


Fig. 1D

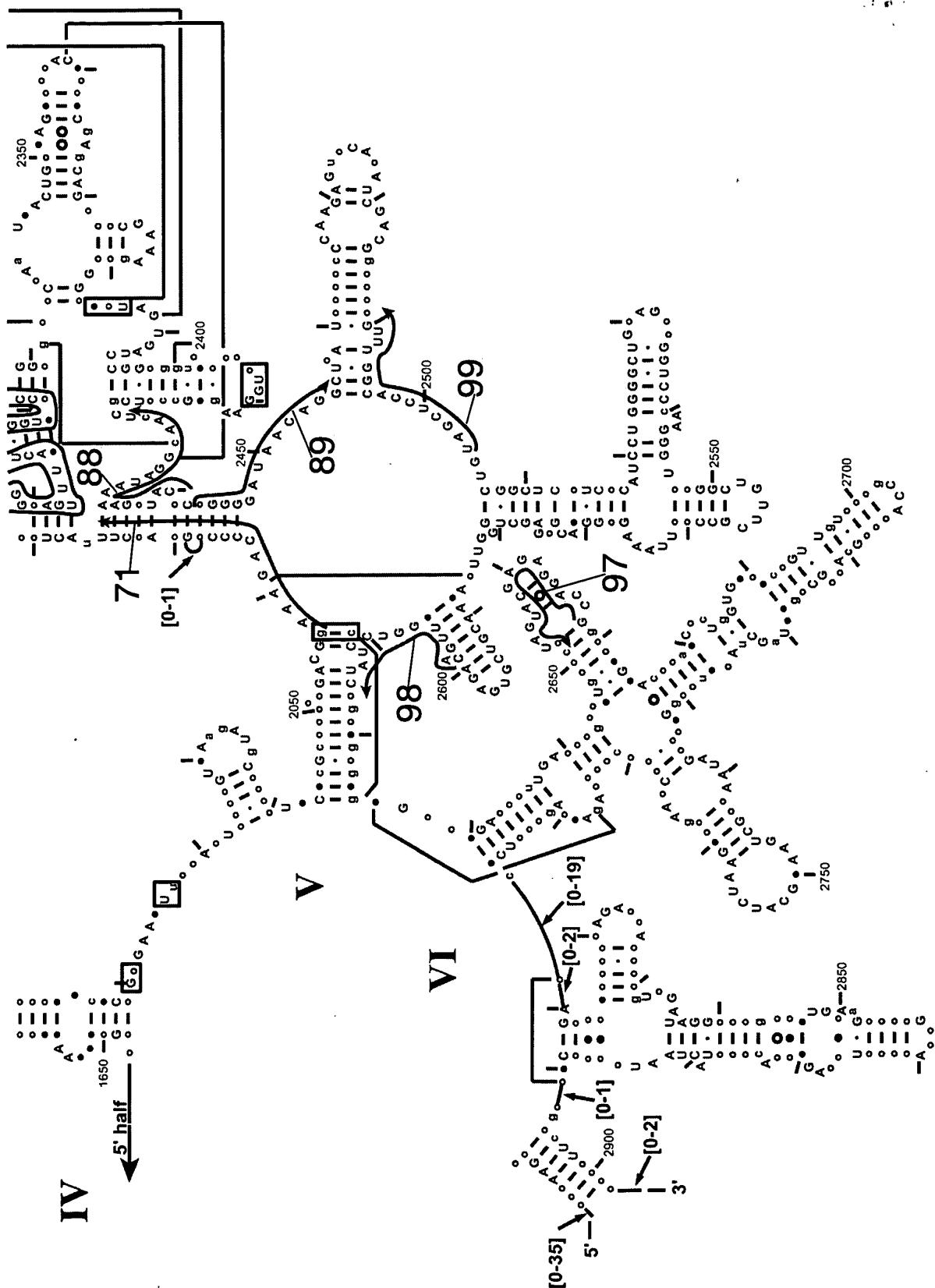


Fig. 1E

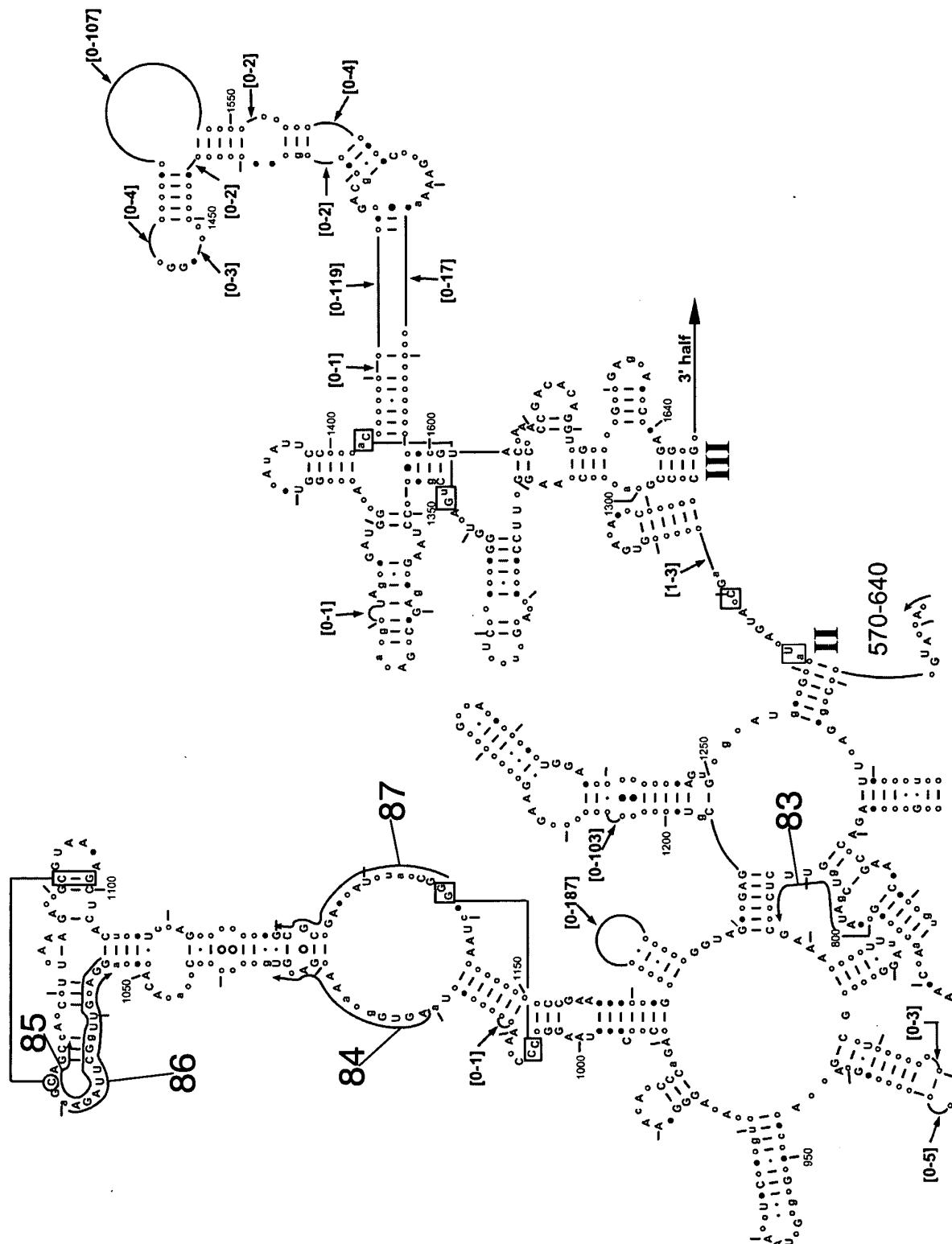


Fig. 1F

APPROVED	O. G. FIG.	SUBCLASS
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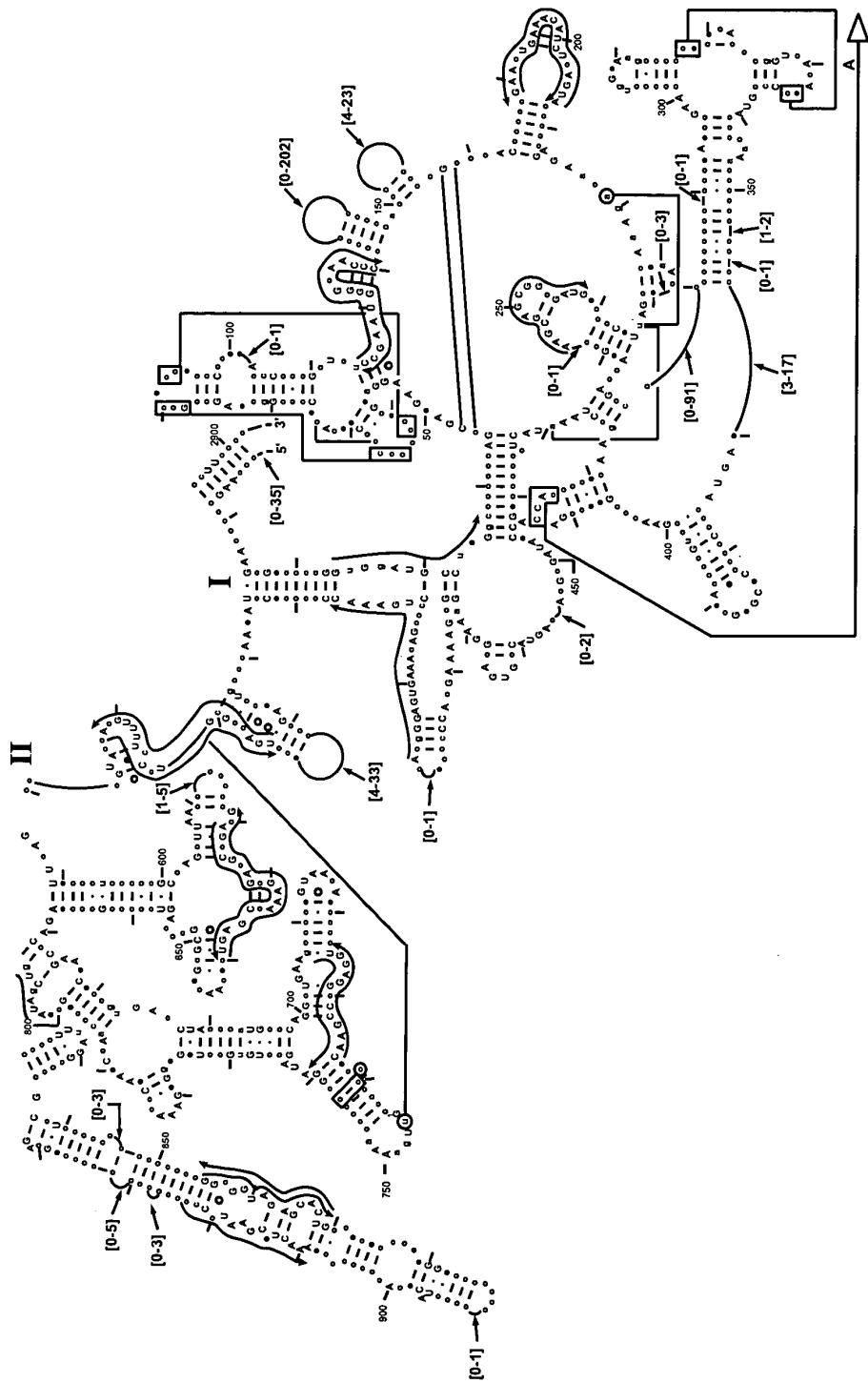


Fig. 1G

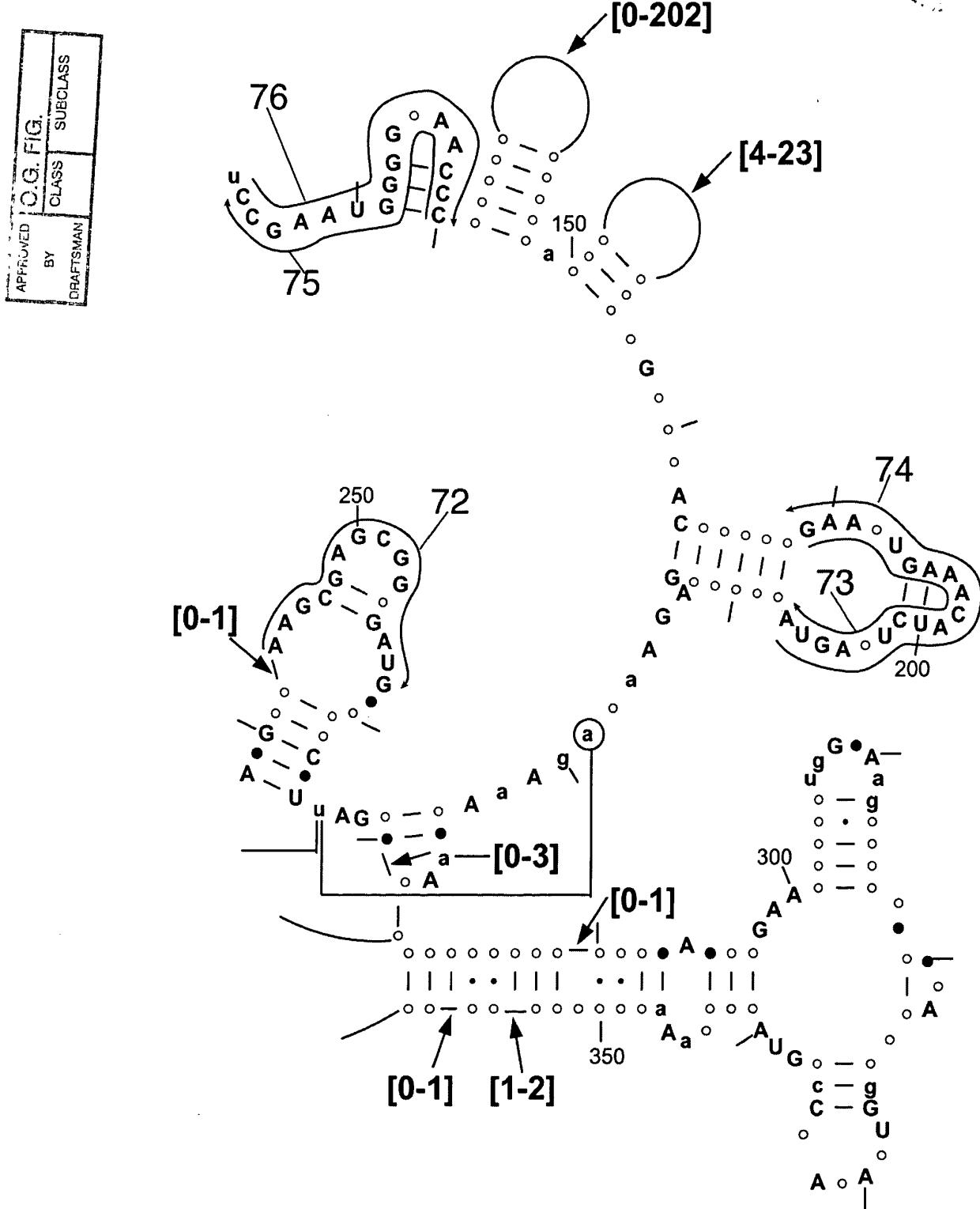


Fig. 1H

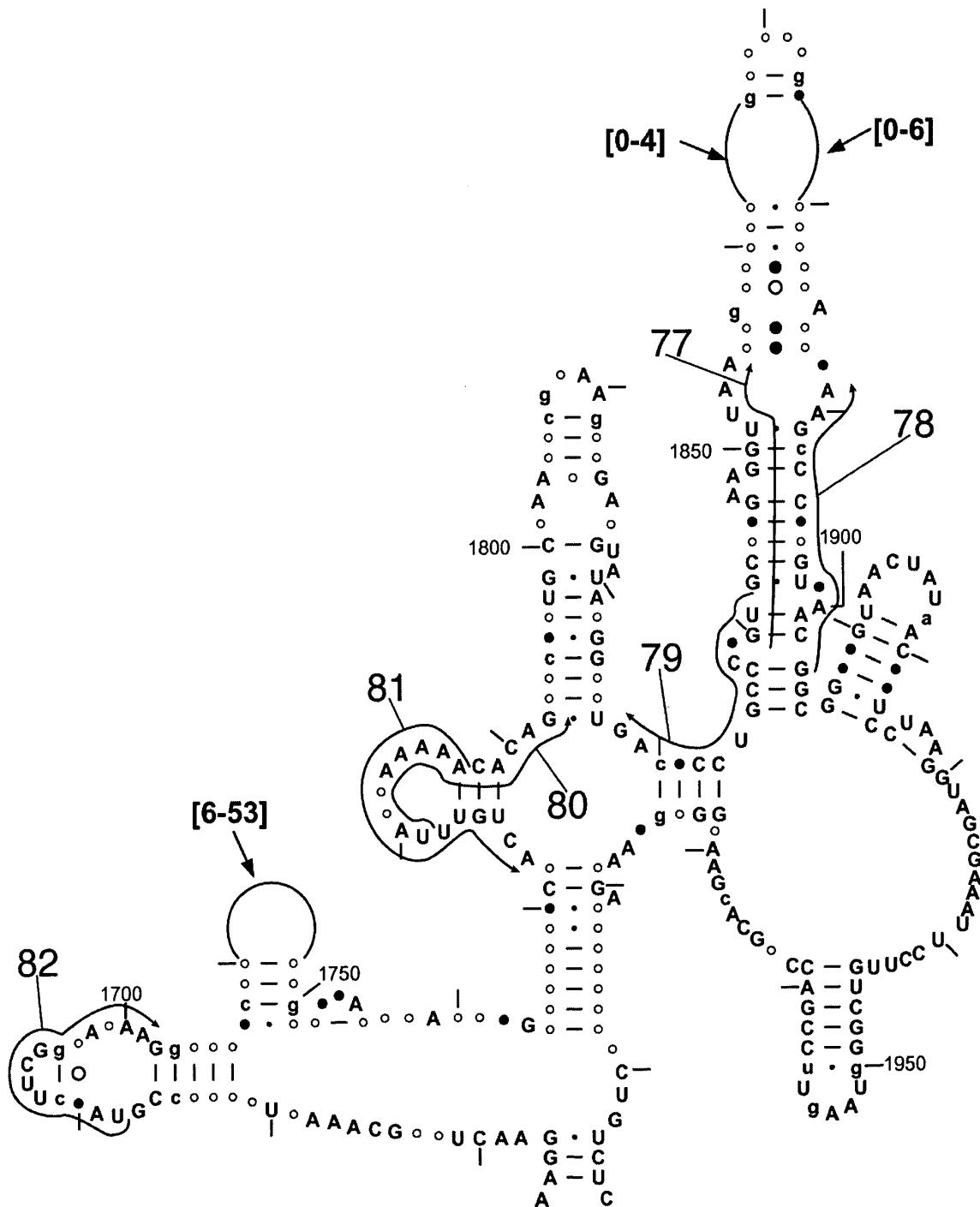


Fig. 2

APPROVED	O. G. FIG.	
BY	CLASS	SUBCLASS
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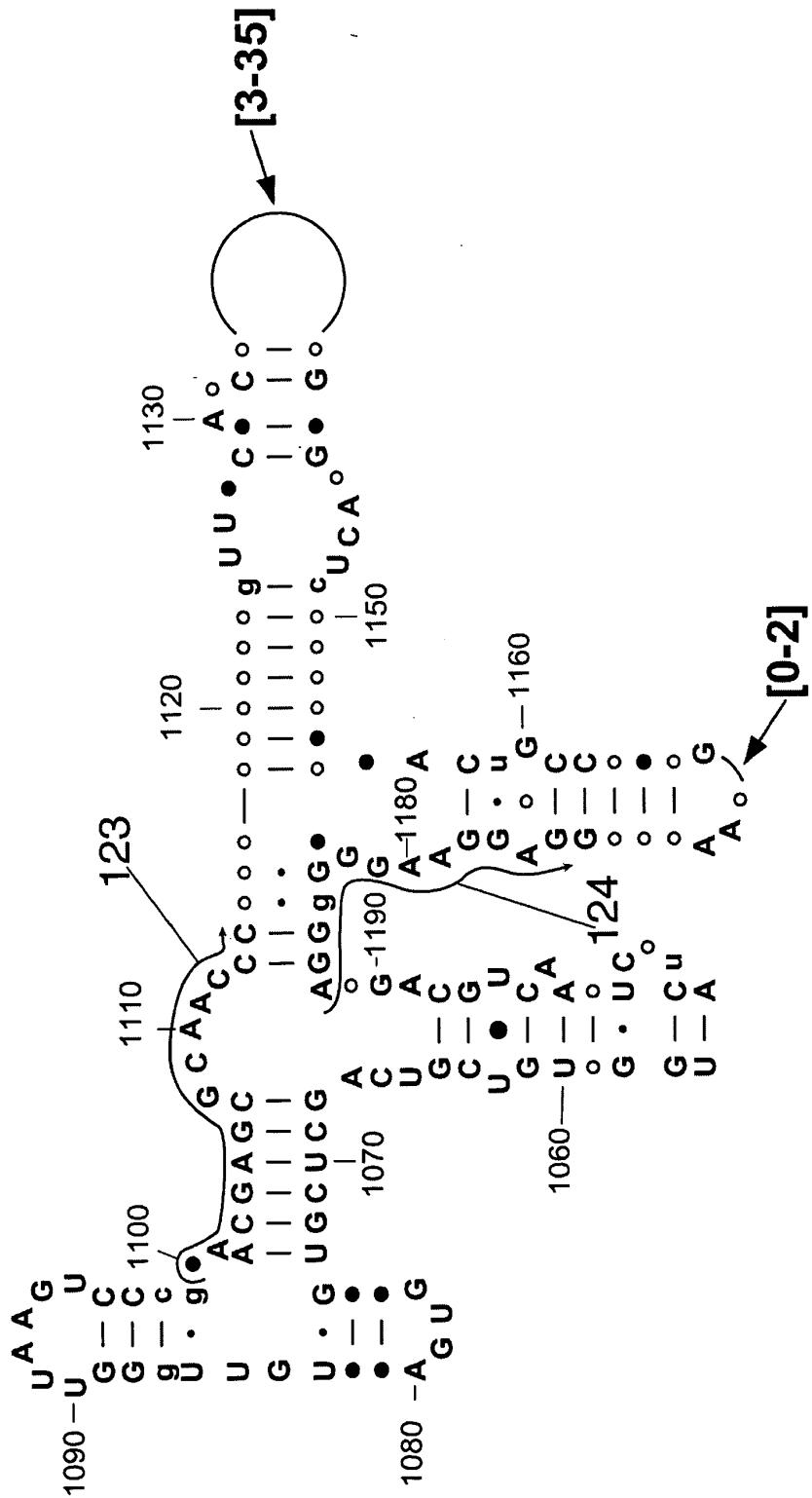
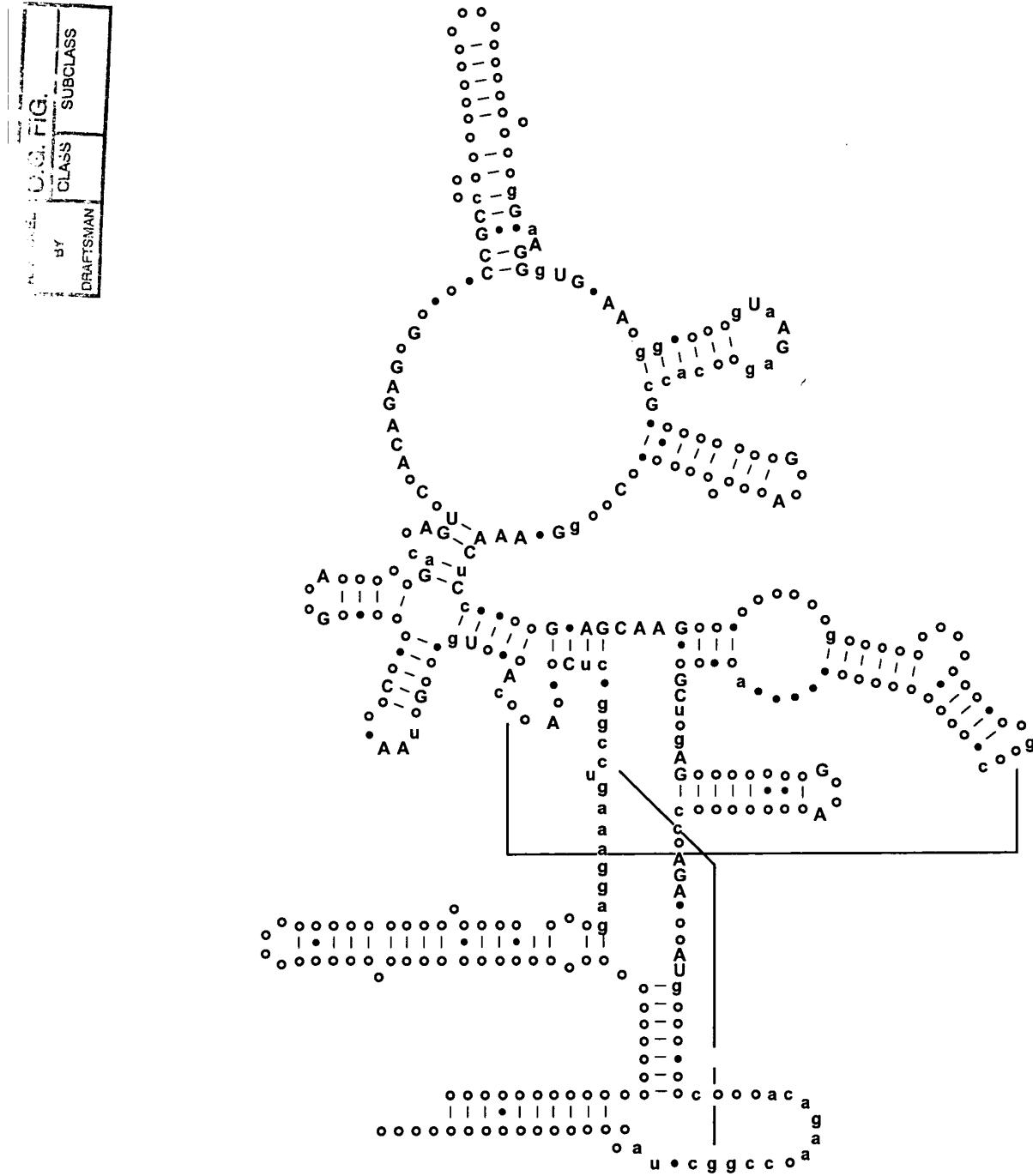


Fig. 3



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Fig. 4

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The diagram illustrates two models for DNA structure. On the left, the 'tag' hypothesis is shown with a sequence: *** tag** **mass (T*-T)=x**. In the center, a DNA duplex is shown with two strands: *** TACGTACGT** and **ATGCATGCA**. An arrow points from the top strand to the right, labeled **(Watson)**. Another arrow points from the bottom strand to the right, labeled **(Crick)**.

* tag mass (C*-C)=y TACGTACGT ATGCATGCA

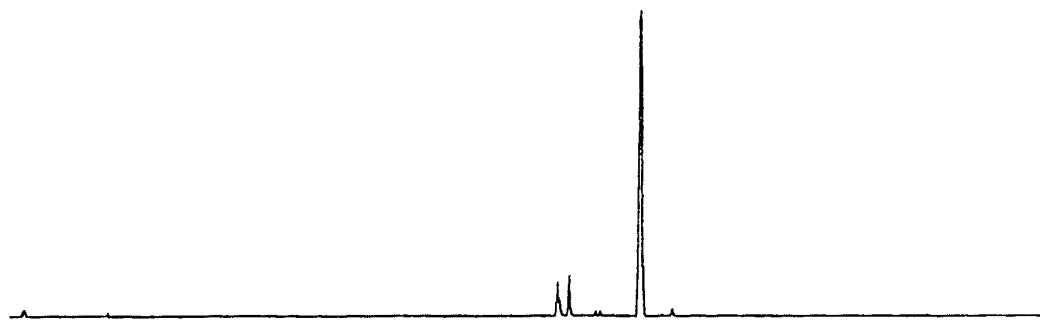
* tag mass (C*-C)=y TACGTACGT ATGCATGCA (Watson)

* tag mass (C*-C)=y TACGTACGT ATGCATGCA (Crick)

Fig. 5

APPROVED	O. G. FIG.	
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B. anthracis ($A_{14}G_9C_{14}T_9$) $MW_{meas} = 14072.2$)



*B. anthracis** ($A_1A^*_{13}G_9C_{14}T_9$) $MW_{meas} = 14280.9$)

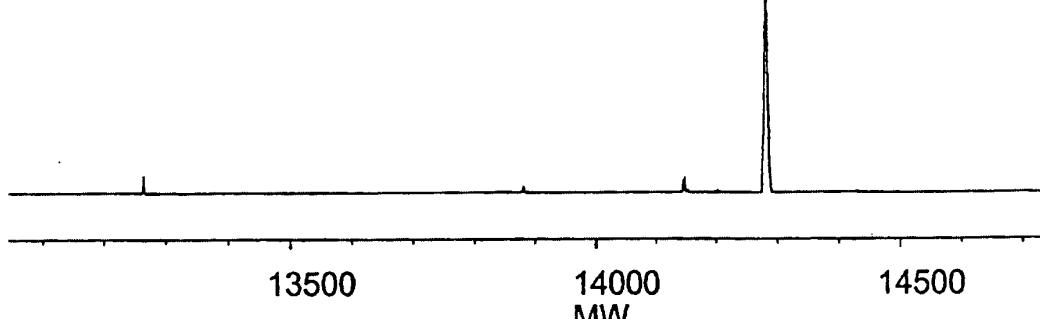


Fig. 6

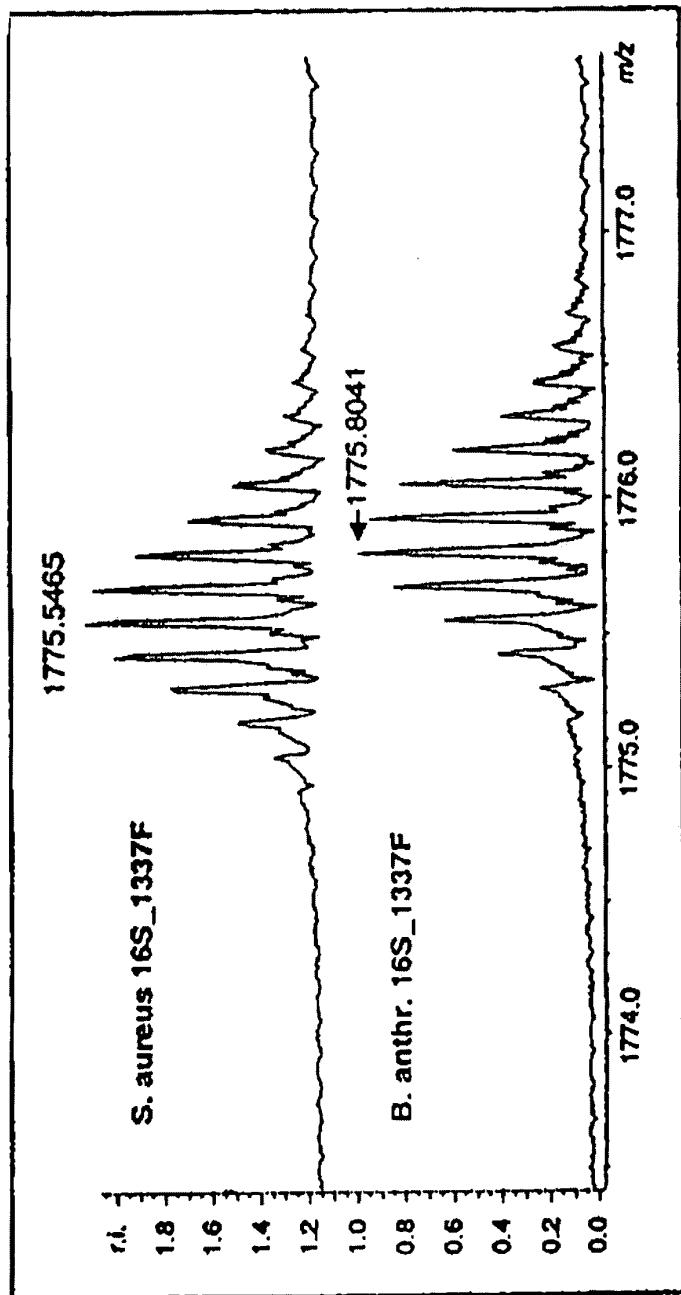
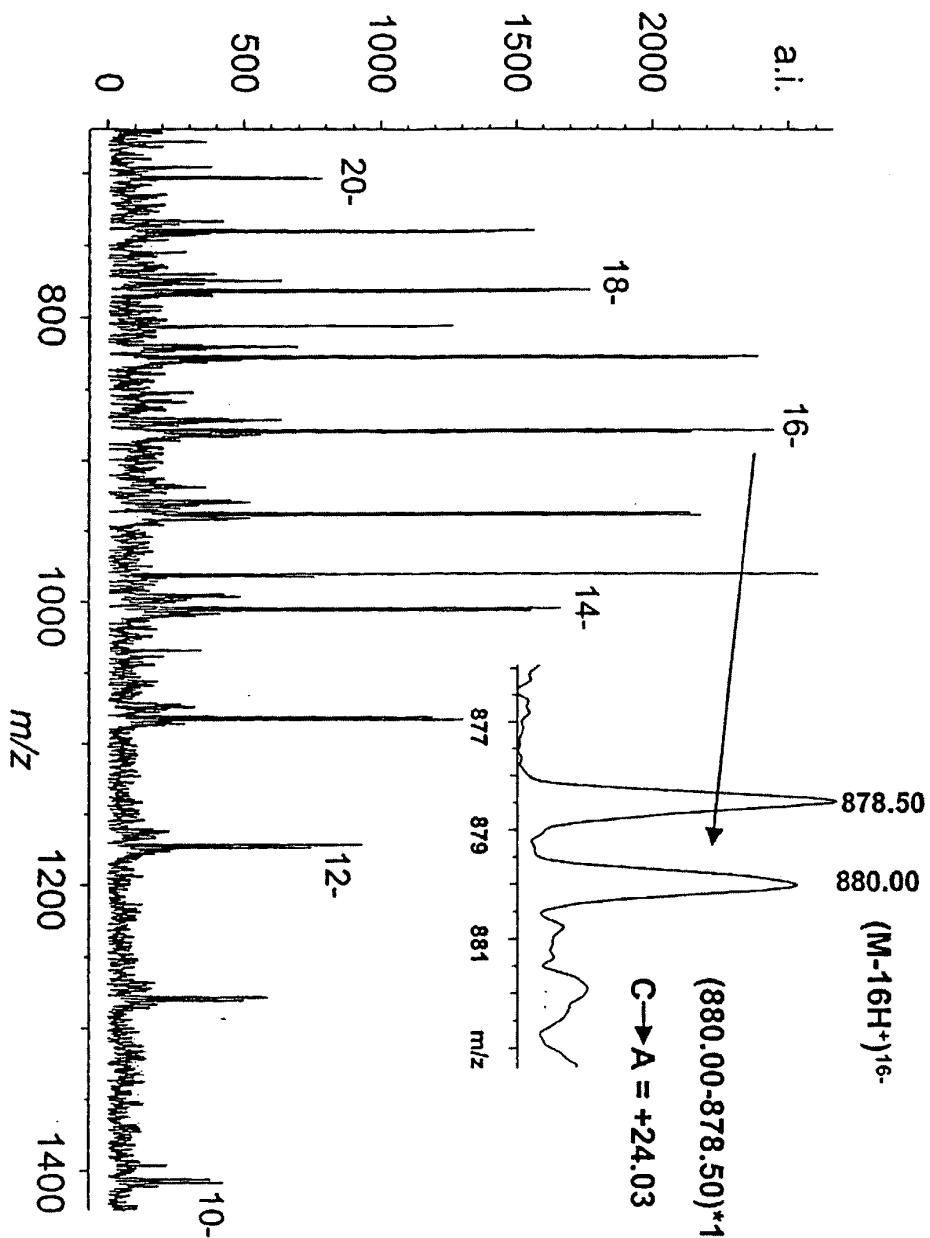


Fig. 7



ESI-TOF MS of sspE 56mer + Calibrant

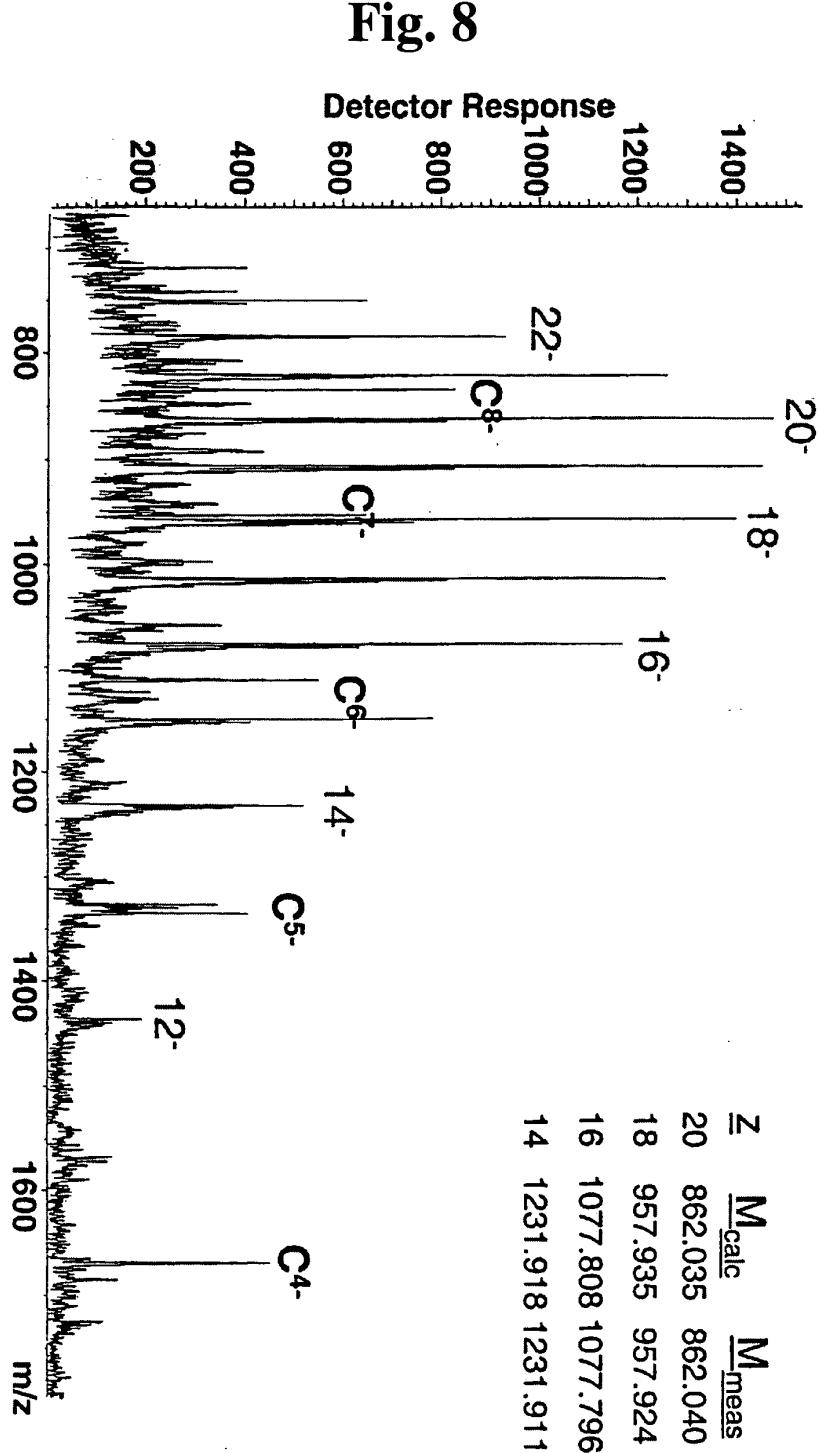
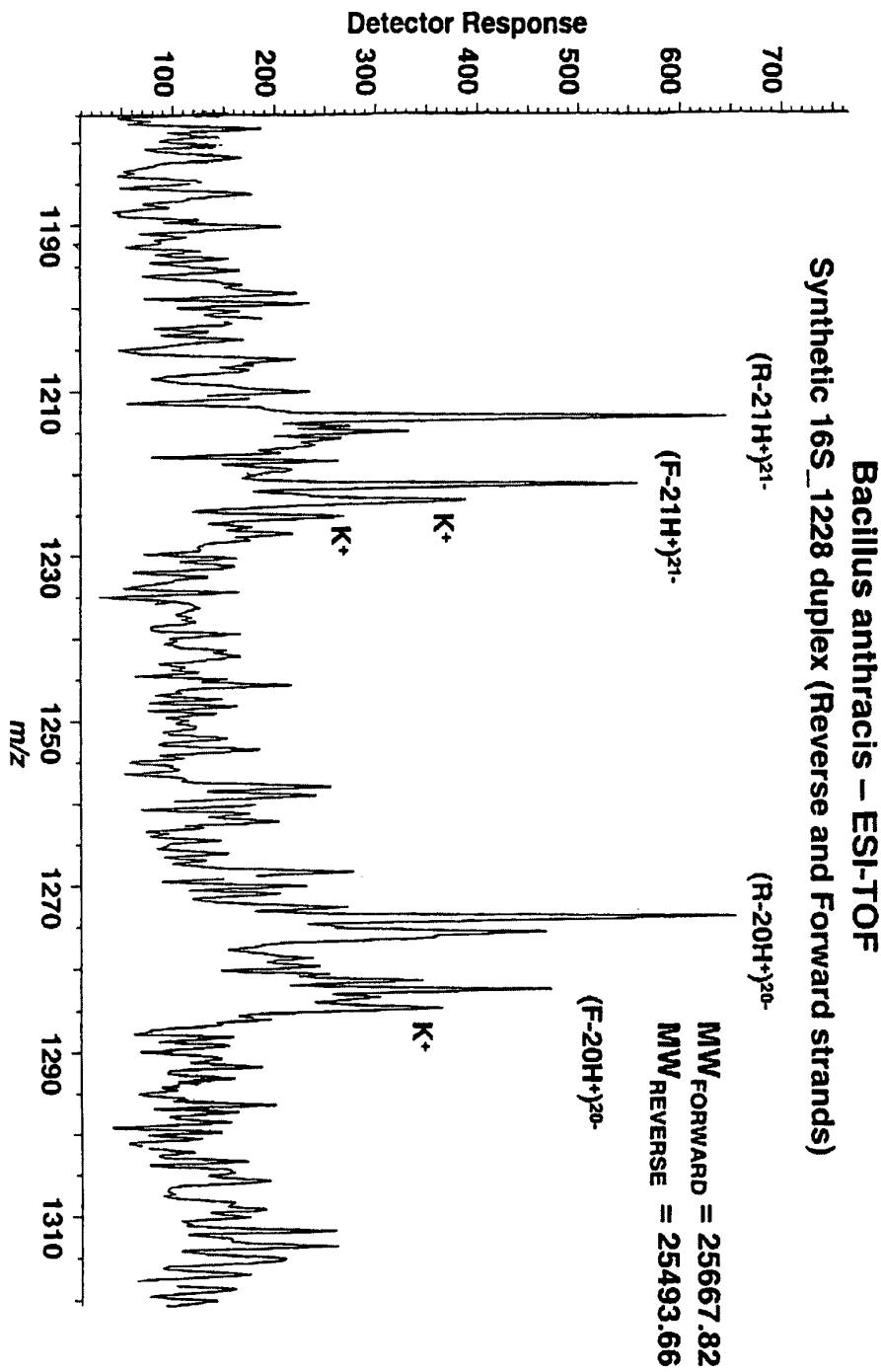


Fig. 9



ESI-FTICR-MS of
Synthetic *Bacillus anthracis* 16S_1337 46 bp duplex

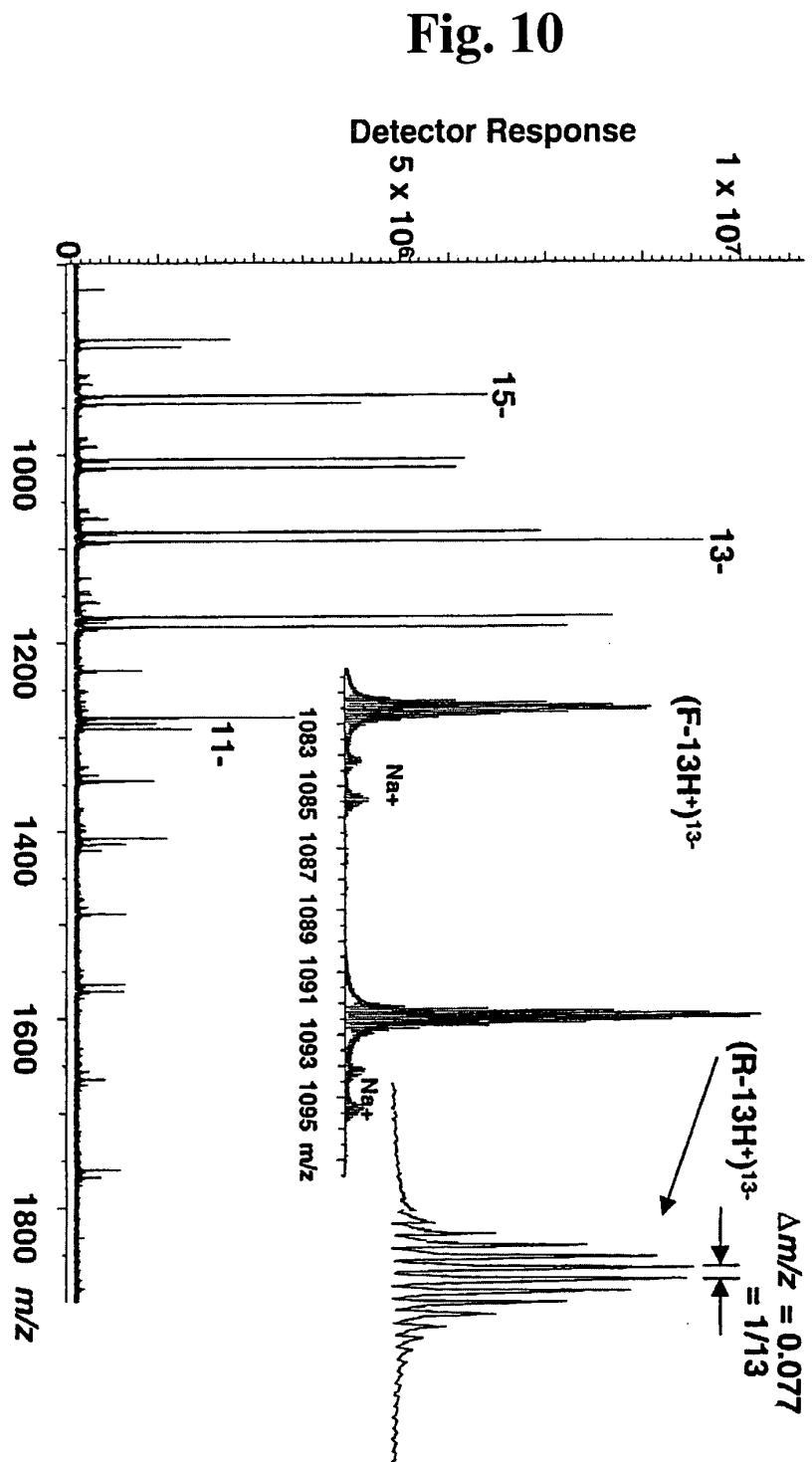


Fig. 11

ESI-TOF-MS of 56-mer BAsb Oligonucleotide
With internal mass standard
ESI at 1.7 μ L/min 5 μ M solution

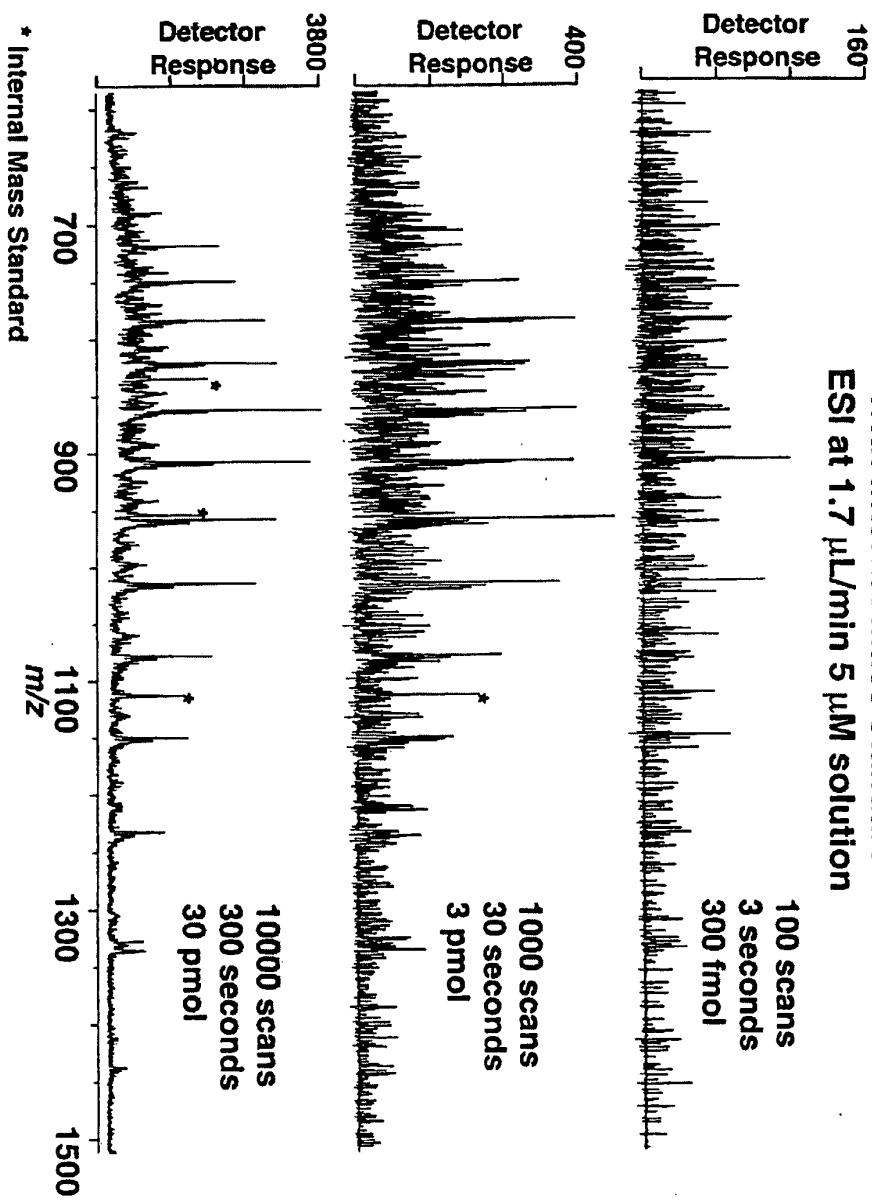


Fig. 12

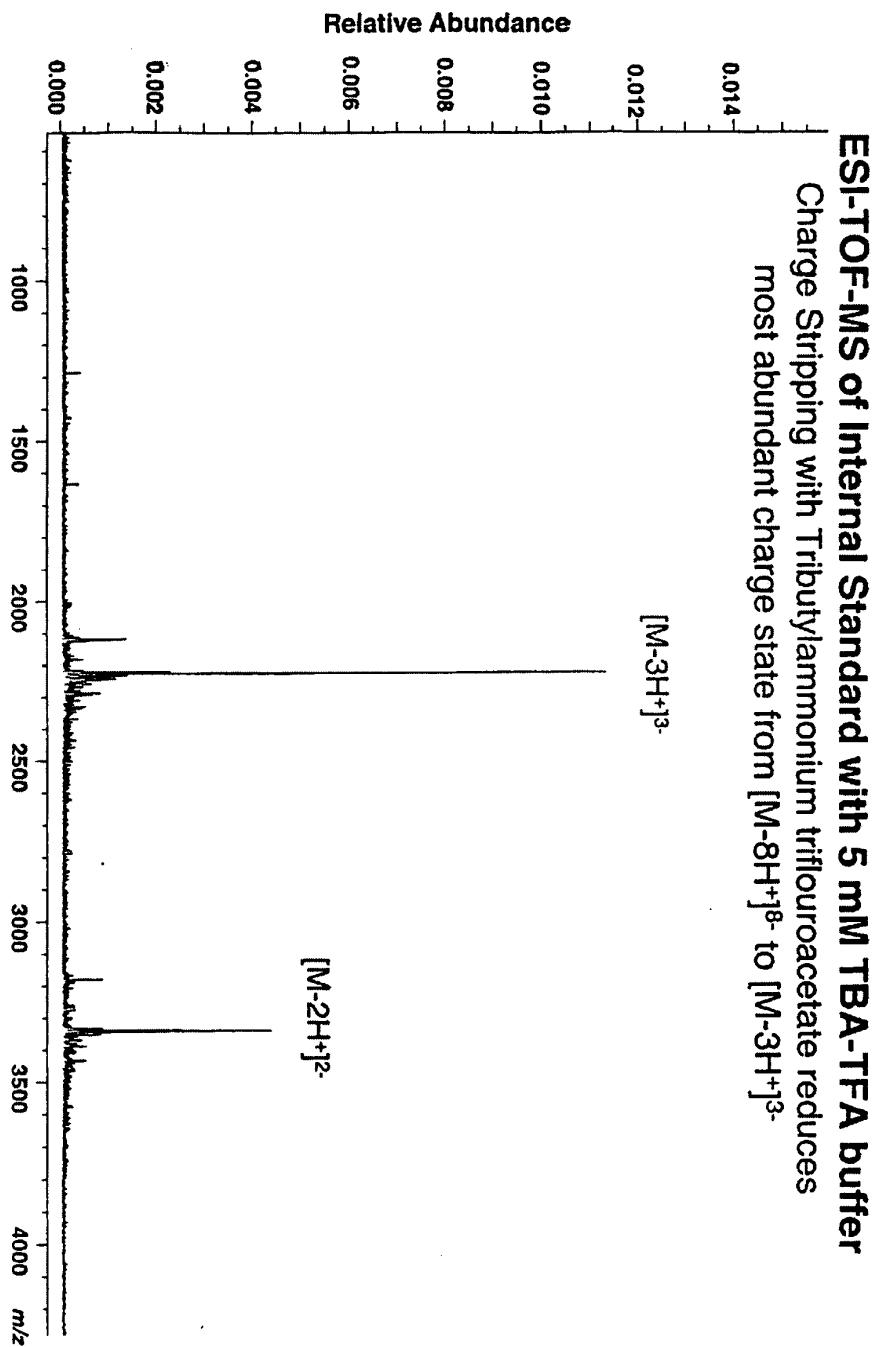
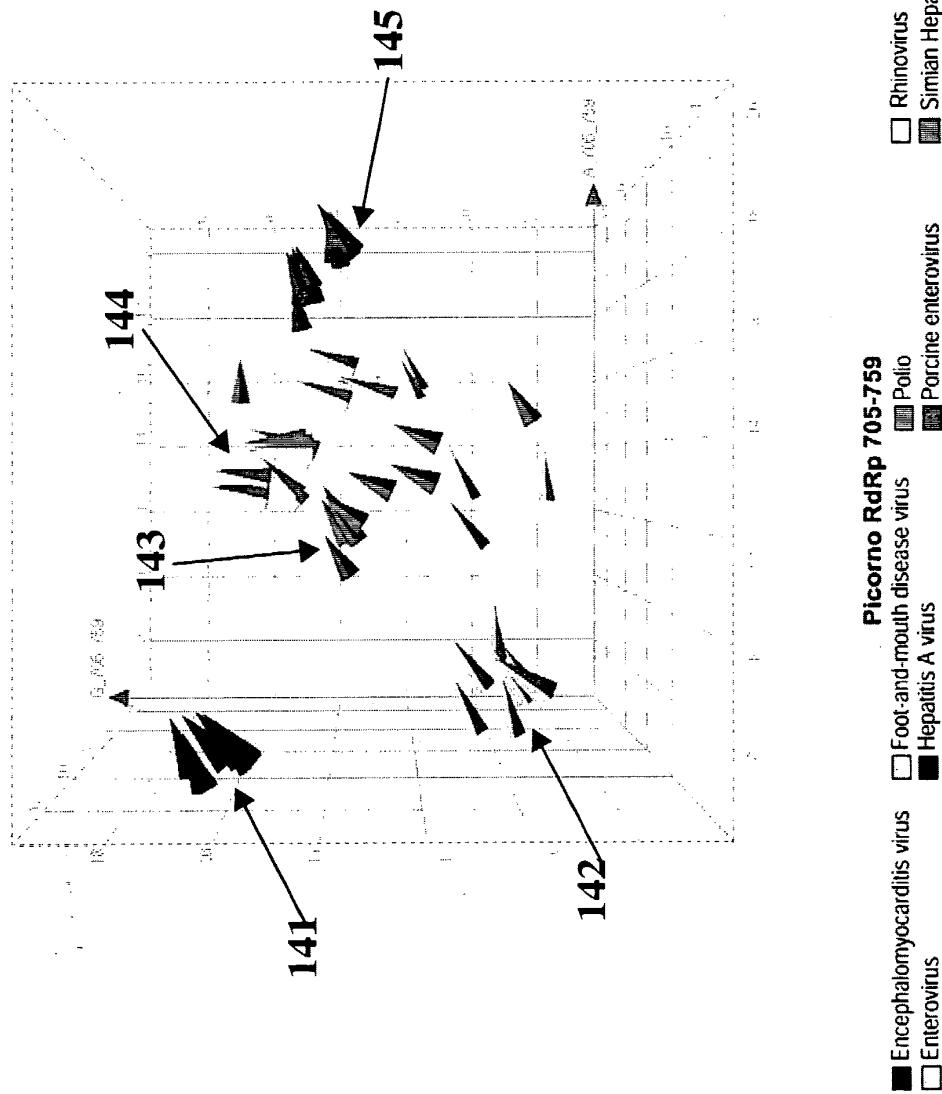


Fig. 13

Diagram illustrating the secondary structure of a ribozyme, showing the arrangement of nucleotides and the locations of 130-nt loops and 131-nt loops. The structure is highly conserved, with many identical nucleotides. Arrows point to the 130-nt loops and 131-nt loops.

APPROVED	O.G. FIG.
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Picornavirus RdRp 705-759

- Encephalomyocarditis virus
- Foot-and-mouth disease virus
- Hepatitis A virus
- Polio
- Porcine enterovirus
- Rhinovirus
- Simian Hepatitis A

Fig. 14

Fig. 15

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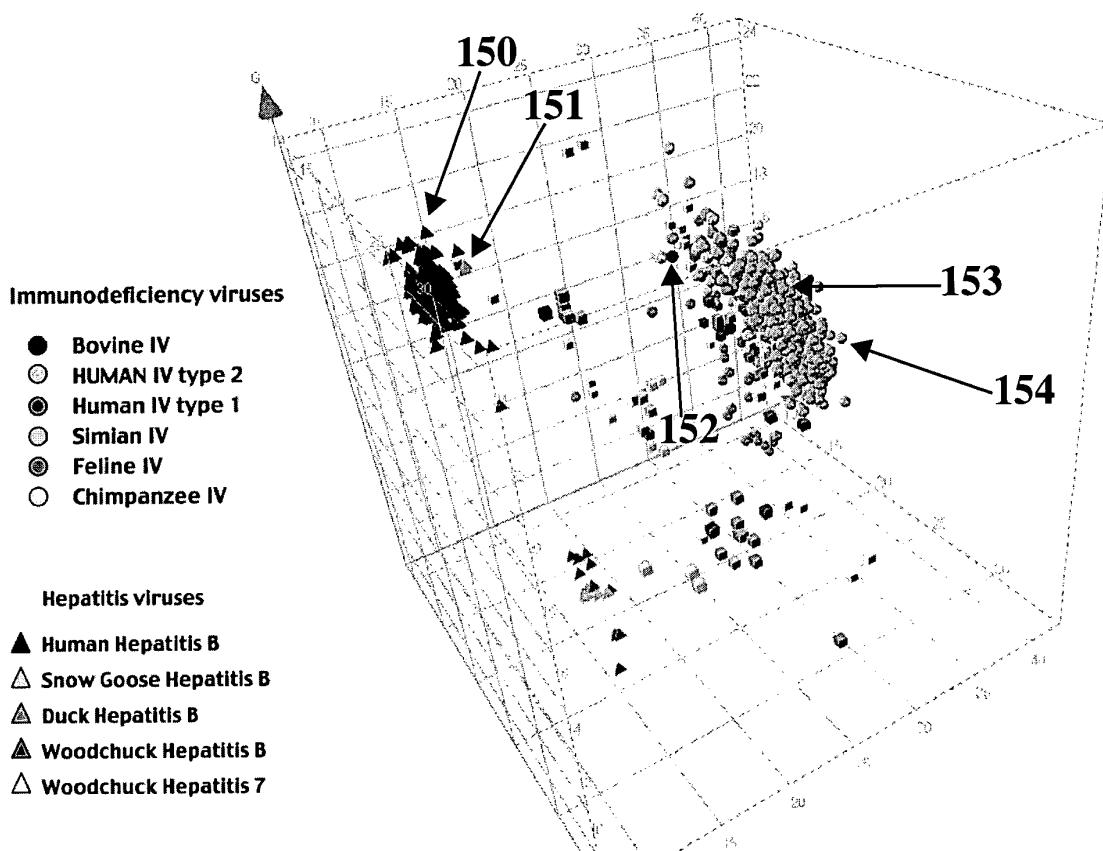
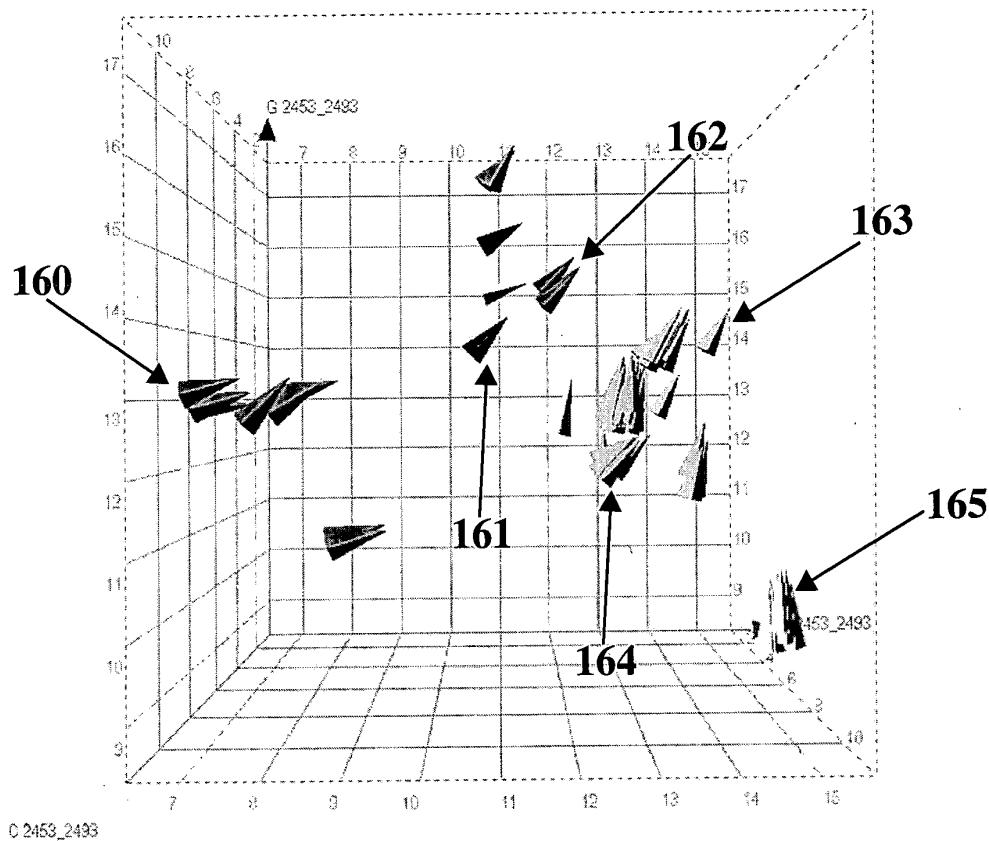


Fig. 16

APPROVED	O.G. FIG.
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Flavi RdRp 2453-2493

<input type="checkbox"/> Dengue virus type	<input type="checkbox"/> Japanese encephalitis virus	<input type="checkbox"/> Tick-borne encephalitis virus
<input type="checkbox"/> Dengue virus type	<input type="checkbox"/> Kunjin virus	<input type="checkbox"/> West Nile virus
<input checked="" type="checkbox"/> Dengue virus type	<input type="checkbox"/> Murray valley encephalitis virus	<input type="checkbox"/> Yellow fever virus

Fig. 17

